

Section C.2

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```
#####
# discrim() is a customized R function to determine discriminant functions.
# By submitting the following lines in R, the function will be defined.
# PLEASE DO NOT BE CONCERNED ABOUT HOW THIS FUNCTION IS DEFINED.
discrim <- function(Y, group){
  Y <- data.matrix(Y)
  group <- as.factor(group)
  m1 <- manova(Y ~ group)
  nu.h <- summary(m1)$stats[1]
  nu.e <- summary(m1)$stats[2]
  p <- ncol(Y)
  SS <- summary(m1)$SS
  E.inv.H <- solve(SS$Residuals) %*% SS$group
  eig <- eigen(E.inv.H)
  s <- min(nu.h, p)
  lambda <- Re(eig$values[1:s])
  a <- Re(eig$vectors[,1:s])
  a.star <- (sqrt(diag(SS$Residuals/nu.e)) * a)
  return(list("a"=a, "a.star"=a.star))
}

#####
# discr.sig() is a customized R function to test significance of discriminant functions.
# By submitting the following lines in R, the function will be defined.
# PLEASE DO NOT BE CONCERNED ABOUT HOW THIS FUNCTION IS DEFINED.
discr.sig <- function(Y, group){
```

```

Y <- data.matrix(Y)
group <- as.factor(group)
m1 <- manova(Y ~ group)
sums <- summary(m1)
evals <- sums$Eigenvalues
nu.e <- m1$df
nu.h <- m1$rank-1
k <- nu.h + 1
p <- ncol(m1$coef)
N <- nu.e + nu.h + 1
s <- min(p, nu.h)
lam <- numeric(s)
dfs <- numeric(s)
for(m in 1:s){
  lam[m] <- prod(1/(1+evals[m:s]))
  dfs[m] <- (p-m+1)*(k-m)
}
V <- -(N - 1 - .5*(p+k))*log(lam)
p.val <- 1 - pchisq(V, dfs)
out <- cbind(Lambda=lam, V, p.values=p.val)
dimnames(out)[[1]] <- paste("LD",1:s,sep="")
return(out)
}

```

```

#####
# partial.f() is a customized R function to test for significance of additional variables.
# By submitting the following lines in R, the function will be defined.
# PLEASE DO NOT BE CONCERNED ABOUT HOW THIS FUNCTION IS DEFINED.
partial.F <- function(Y, group){
  Y <- data.matrix(Y)
  group <- as.factor(group)
  p <- ncol(Y)
  m1 <- manova(Y ~ group)
  nu.e <- m1$df
  nu.h <- m1$rank-1
  Lambda.p <- summary(m1,test="Wilks")$stats[3]
  Lambda.p1 <- numeric(p)
  for(i in 1:p){
    dat <- data.matrix(Y[,-i])
    m2 <- manova(dat ~ group)
    Lambda.p1[i] <- summary(m2,test="Wilks")$stats[3]
  }
}

```

```

Lambda <- Lambda.p / Lambda.p1
F.stat <- ((1 - Lambda) / Lambda) * ((nu.e - p + 1)/nu.h)
p.val <- 1 - pf(F.stat, nu.h, nu.e - p + 1)
out <- cbind(Lambda, F.stat, p.value = p.val)
dimnames(out)[[1]] <- dimnames(Y)[[2]]
ord <- rev(order(out[,2]))
return(out[ord,])
}

```

#####

```

# discr.plot() is a customized R function to visualize discriminant functions.
# By submitting the following lines in R, the function will be defined.
# PLEASE DO NOT BE CONCERNED ABOUT HOW THIS FUNCTION IS DEFINED.

```

```

discr.plot <- function(Y, group, leg = NULL){
a <- discrim(Y, group)$a
z <- data.matrix(Y) %*% a
plot(z[,1], z[,2], type = "n", xlab = "LD1", ylab="LD2")
for(i in 1:length(unique(group))){
points(z[group == unique(group)[i],1],
z[group == unique(group)[i],2], pch = i)
}
if(is.null(leg)) leg <- as.character(unique(group))
legend("topright",legend = leg,pch=1:length(unique(group)))
}

```

#####

```

lin.class <- function(Y,group){
# Install MASS package if not already installed
if (!require("MASS")) install.packages("MASS")
library(MASS)
Y <- data.matrix(Y)
group <- as.factor(group)
p <- ncol(Y)
m1 <- manova(Y ~ group)
nu.e <- m1$df
nu.h <- m1$rank-1
Sp <- summary(m1)$SS$Residual/(nu.e)
cio <- 1:m1$rank
c.mat <- matrix(nrow=m1$rank,ncol=p,0)
for (i in 1:m1$rank) {
cio[i] <- -.5*t(lda(Y,group)$means[i,])%*%solve(Sp)%*%
lda(Y,group)$means[i,]
c.mat[i,] <- t(lda(Y,group)$means[i,])%*%solve(Sp)
}
}

```

```

}
return(list("coefs"=c.mat,"c.0"=cio))
}
#####
rates <- function(data,group,method="l") {
  if (!require("MASS")) install.packages("MASS")
  library(MASS)
  data <- as.matrix(data)
  group <- as.matrix(group)
  da.obj <- lda(data,group)
  if (method=="q") {
    da.obj <- qda(data,group)
    method <- "QDA"
  }
  tab <- table(original=group,predicted=predict(da.obj)$class)
  if (method=="l") method <- "LDA"
  cor.rate <- sum(predict(da.obj)$class==group)/nrow(data)
  er.rate <- 1-cor.rate
  return(list("Correct Class Rate"=cor.rate,"Error Rate"=er.rate,
    "Method"=method,"Confusion Matrix"=tab))
}

```

C.2: Discriminant Analysis

Discriminant Functions and Variable Importance

```

nhanes <- read.csv("NHANES3_419.csv")
nhanes$SBPRANK <- as.factor(nhanes$SBPRANK)

# Omit height variable
nhanes <- nhanes[, c("SBPRANK", "HSAGEIR", "BMPWTLBS", "PEPMNK5R", "TCP")]

X <- nhanes[, -1]
y <- nhanes[, 1]

discrim(X, y)$a.stand

```

```

      [,1]      [,2]
[1,] -10.784324 -8.677779
[2,]  -3.772346  7.113163

```

```
[3,] -7.754878  8.769770
[4,]  2.881487  2.341885
```

Let:

- y_1 = HSAGEIR (Age) (variable 2)
- y_2 = BMPWTLBS (Body Weight) (variable 3)
- y_3 = PEPMNK5R (Average Diastolic BP) (variable 5)
- y_4 = TCP (Serum Cholesterol) (variable 6)

Then the standardized discriminant functions are:

$$LD_1(y) = -10.784y_1 - 3.772y_2 - 7.755y_3 + 2.881y_4$$

$$LD_2(y) = -8.678y_1 + 7.113y_2 + 8.770y_3 + 2.342y_4$$

We now rank the standardized coefficients of each discriminant function, LD_1 and LD_2 , by observing their absolute values.

For the first discriminant function (LD_1), y_1 (age) and y_3 (average diastolic BP) are the most important for separating the groups, followed by y_2 (body weight) and y_4 (cholesterol): $y_1 \rightarrow y_3 \rightarrow y_2 \rightarrow y_4$.

For the second discriminant function (LD_2), y_3 , y_1 , and y_2 are the most important, followed by y_4 : $y_3 \rightarrow y_1 \rightarrow y_2 \rightarrow y_4$.

Significance Tests for Discriminant Functions

```
discr.sig(X, y)
```

	Lambda	V	p.values
LD1	0.4856068	147.721810	0.00000000
LD2	0.9596942	8.413261	0.03820007

Using an adjusted significance level of $\alpha^* = \frac{0.05}{2} = 0.025$, we assess the significance of each discriminant function.

- H_0 : $\alpha_1 = \alpha_2 = 0$
- H_a : At least one $\alpha_i \neq 0$

For the first test, the p-value is less than 0.0001, which is well below the adjusted significance level. We therefore reject the null hypothesis and conclude that at least one of the discriminant functions significantly separates the SBPRANK groups.

- $H_0: \alpha_2 = 0$
- $H_a: \alpha_2 \neq 0$

For the second test, the p-value is 0.0382, which is greater than the adjusted significance level of 0.025. Therefore, we fail to reject the null hypothesis and conclude that LD_2 does not provide significant additional separation beyond LD_1 .

Significance Tests for Additional Variables

```
partial.F(X, y)
```

	Lambda	F.stat	p.value
HSAGEIR	0.6046790	66.357652	0.000000e+00
PEPMNK5R	0.7659335	31.018029	1.759481e-12
BMPWTLBS	0.9344024	7.125580	1.021397e-03
TCP	0.9679940	3.356017	3.681948e-02

Using the an adjusted significance level of $\alpha^* = \frac{0.05}{4} = 0.0125$ to account for the presence of other non-grouping variables, we assess the significance of each non-grouping variable.

- H_0 : HSAGEIR does not contribute to group separation after accounting for the other variables.
- H_a : HSAGEIR contributes significantly to group separation.

For HSAGEIR (age), the p-value is less than 0.0001, which is below the adjusted significance level. We therefore reject the null hypothesis and conclude that age contributes significantly to the separation of SBPRANK groups.

- H_0 : PEPMNK5R does not contribute to group separation after accounting for the other variables.
- H_a : PEPMNK5R contributes significantly to group separation.

For PEPMNK5R (average diastolic blood pressure), the p-value is approximately 1.76×10^{-12} , which is also far below the adjusted threshold. We therefore reject the null hypothesis and conclude that diastolic blood pressure significantly contributes to group separation.

- H_0 : BMPWTLBS does not contribute to group separation after accounting for the other variables.

- H_a : BMPWTLBS contributes significantly to group separation.

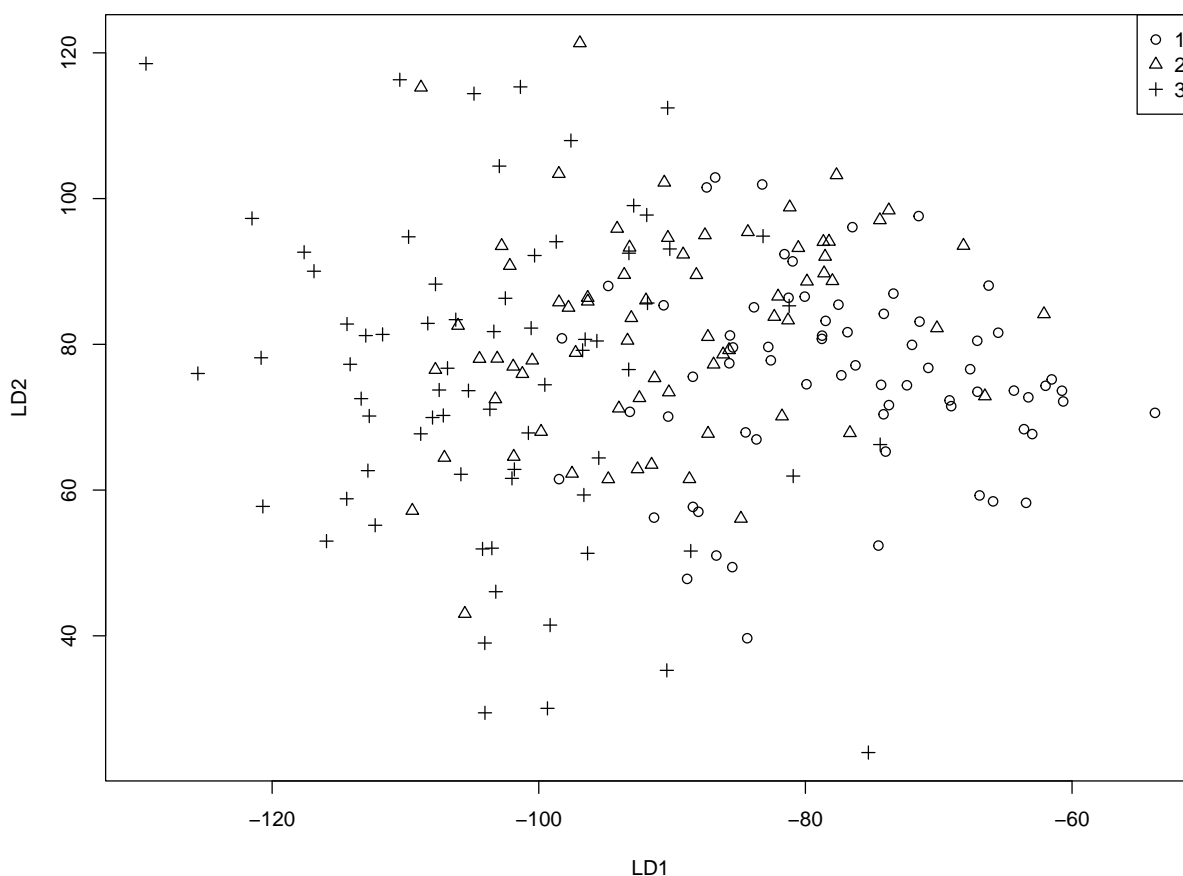
For BMPWTLBS (body weight), the p-value is 0.00102, which is below the adjusted significance level. We therefore reject the null hypothesis and conclude that body weight contributes significantly to distinguishing between groups.

- H_0 : TCP does not contribute to group separation after accounting for the other variables.
- H_a : TCP contributes significantly to group separation.

For TCP (serum cholesterol), the p-value is 0.0368, which exceeds the adjusted significance level. We therefore fail to reject the null hypothesis and conclude that cholesterol does not provide a significant contribution to group separation after accounting for the other variables.

Visualizing Discriminant Functions

```
discr.plot(X, y)
```



The above discriminant plot supports the results of our analysis, showing that the first linear discriminant function provides clearer separation between the SBPRANK groups than the second. Most notably, along the LD_1 axis, there appears to be greater separation of groups 1 and 3, corresponding to individuals with average systolic blood pressure less than or equal to 116 and those with values greater than 131, respectively. On the other hand, separation along LD_2 's axis is comparatively limited.